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SEQUENCE LISTING

<110> THE CORPORATION OF THE TRUSTEES OF THE ORDER OF THE SISTERS OF
MERCY IN QUEENSLAND

<120> NOVEL THERAPEUTIC MOLECULES AND USES THEREOF

<130> 12381870/TDO

<150> 2002953223

<151> 2002-06-12

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 5622

<212> DNA

<213> mammalian

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<221> CDS

<222> (1)..(5619)

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Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala	
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aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag	144
Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys	
35 40 45	
cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac	192
Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp	
50 55 60	
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Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser	
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Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg	
85 90 95	
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Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His	
100 105 110	

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cat ggc aca gca atc tca aat gca tct gat gtc tgg aag aaa gga ggc His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly 130 135 140	432
tca gag gaa agc ctt tgt gac cag cct tat cat gag atc tat acc aga Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg 145 150 155 160	480
gat ggg aac tct tat ggg aga cct tgt gaa ttt cca ttc tta att gat Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp 165 170 175	528
ggg acc tgg cat cat gat tgc att ctt gat gaa gat cat agt ggg cca Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro 180 185 190	576
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tgc tta aag cct gaa aac ggt tgt gaa gat aat tgg gaa aag aac gag Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu 210 215 220	672
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gca cat gcg aaa tgc aaa gcc ttc agt agt gac cta atc agc att cat Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His 385 390 395 400	1200
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atc aaa gaa gaa gtg tgg ata ggc ctt aag aac ata aac ata cca act Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr 420 425 430	1296
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cct gtg aca ttt gga gag gaa tgc ttg tac atg tct gcc aag act tgg Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp 900 905 910	2736
ctt atc gac tta ggt aaa cca aca gac tgt agt acc aag ttg ccc ttc Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe 915 920 925	2784
atc tgt gaa aaa tat aat gtt tct tcg tta gag aaa tac agc cca gat Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp 930 935 940	2832
tct gca gct aaa gtg caa tgt tct gag caa tgg att cct ttt cag aat Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn 945 950 955 960	2880
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cag att gaa caa gac ttt att aca tcc ttg ctt ccg gat atg gaa gct Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala 995 1000 1005	3024

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Thr Leu Trp Ile Gly Leu Arg	Trp Thr Ala Tyr Glu	Lys Ile Asn	
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aaa tgg aca gat aac aga gag	ctg acg tac agt aac	ttt cac cca	3114
Lys Trp Thr Asp Asn Arg Glu	Leu Thr Tyr Ser Asn	Phe His Pro	
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tta ttg gtt agt ggg agg ctg	aga ata cca gaa aat	ttt ttt gag	3159
Leu Leu Val Ser Gly Arg Leu	Arg Ile Pro Glu Asn	Phe Phe Glu	
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gaa gag tct cgc tac cac tgt	gcc cta ata ctc aac	ctc caa aaa	3204
Glu Glu Ser Arg Tyr His Cys	Ala Leu Ile Leu Asn	Leu Gln Lys	
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Ser Pro Phe Thr Gly Thr Trp	Asn Phe Thr Ser Cys	Ser Glu Arg	
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cac ttt gtg tct ctc tgt cag	aaa tat tca gaa gtt	aaa agc aga	3294
His Phe Val Ser Leu Cys Gln	Lys Tyr Ser Glu Val	Lys Ser Arg	
1085	1090	1095	
cag acg ttg cag aat gct tca	gaa act gta aag tat	cta aat aat	3339
Gln Thr Leu Gln Asn Ala Ser	Glu Thr Val Lys Tyr	Leu Asn Asn	
1100	1105	1110	
ctg tac aaa ata atc cca aag	act ctg act tgg cac	agt gct aaa	3384
Leu Tyr Lys Ile Ile Pro Lys	Thr Leu Thr Trp His	Ser Ala Lys	
1115	1120	1125	
agg gag tgt ctg aaa agt aac	atg cag ctg gtg agc	atc acg gac	3429
Arg Glu Cys Leu Lys Ser Asn	Met Gln Leu Val Ser	Ile Thr Asp	
1130	1135	1140	
cct tac cag cag gca ttc ctc	agt gtg cag gcg ctc	ctt cac aac	3474
Pro Tyr Gln Gln Ala Phe Leu	Ser Val Gln Ala Leu	Leu His Asn	
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Ser Ser Leu Trp Ile Gly Leu	Phe Ser Gln Asp Asp	Glu Leu Asn	
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Phe Gly Trp Ser Asp Gly Lys	Arg Leu His Phe Ser	Arg Trp Ala	
1175	1180	1185	
gaa act aat ggg caa ctc gaa	gac tgt gta gta tta	gac act gat	3609
Glu Thr Asn Gly Gln Leu Glu	Asp Cys Val Val Leu	Asp Thr Asp	
1190	1195	1200	
gga ttc tgg aaa aca gtt gat	tgc aat gac aat caa	cca ggt gct	3654
Gly Phe Trp Lys Thr Val Asp	Cys Asn Asp Asn Gln	Pro Gly Ala	
1205	1210	1215	

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Val Asp	Ser Val Lys Cys Pro	Ser Pro Val Leu Asn	Thr Pro Trp	
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ata cca	ttt cag aac tgt tgc	tac aat ttc ata ata	aca aag aat	3789
Ile Pro	Phe Gln Asn Cys Cys	Tyr Asn Phe Ile Ile	Thr Lys Asn	
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agg cat	atg gca aca aca cag	gat gaa gtt cat act	aaa tgc cag	3834
Arg His	Met Ala Thr Thr Gln	Asp Glu Val His Thr	Lys Cys Gln	
1265	1270	1275		
aaa ctg	aat cca aaa tca cat	att ctg agt att cga	gat gaa aag	3879
Lys Leu	Asn Pro Lys Ser His	Ile Leu Ser Ile Arg	Asp Glu Lys	
1280	1285	1290		
gag aat	aac ttt gtt ctt gag	caa ctg ctg tac ttc	aat tat atg	3924
Glu Asn	Asn Phe Val Leu Glu	Gln Leu Leu Tyr Phe	Asn Tyr Met	
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gct tca	tgg gtc atg tta gga	ata act tat aga aat	aat tct ctt	3969
Ala Ser	Trp Val Met Leu Gly	Ile Thr Tyr Arg Asn	Asn Ser Leu	
1310	1315	1320		
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Met Trp	Phe Asp Lys Thr Pro	Leu Ser Tyr Thr His	Trp Arg Ala	
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Gly Arg	Pro Thr Ile Lys Asn	Glu Lys Phe Leu Ala	Gly Leu Ser	
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Thr Asp	Gly Phe Trp Asp Ile	Gln Thr Phe Lys Val	Ile Glu Glu	
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Ala Val	Tyr Phe His Gln His	Ser Ile Leu Ala Cys	Lys Ile Glu	
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Met Pro	Tyr Glu Asp Gly Ile	Tyr Ser Val Ile Gln	Lys Lys Val	
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aca tgg	tat gaa gca tta aac	atg tgt tct caa agt	gga ggt cac	4284
Thr Trp	Tyr Glu Ala Leu Asn	Met Cys Ser Gln Ser	Gly Gly His	
1415	1420	1425		

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Phe Gly Arg Val Val Cys Lys	Val Pro Leu Asp Cys	Pro Ser Ser	
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gcc atc aaa gta gaa agc ata	gag gat gtc aga aat	cag tgt act	5094
Ala Ile Lys Val Glu Ser Ile	Glu Asp Val Arg Asn	Gln Cys Thr	
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Asp His Gly Ala Asp Met Ile	Ser Ile His Asn Glu	Glu Glu Asn	
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Ala Phe Ile Leu Asp Thr Leu	Lys Lys Gln Trp Lys	Gly Pro Asp	
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Lys Trp Phe Asp Asn Ser Asn	Met Thr Phe Asp Lys	Trp Thr Asp	
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caa gat gat gat gag gat tta	gtt gac acc tgt gct	ttt ctg cac	5319
Gln Asp Asp Asp Glu Asp Leu	Val Asp Thr Cys Ala	Phe Leu His	
1760	1765	1770	
atc aag aca ggt gaa tgg aaa	aaa gga aat tgt gaa	gtt tct tct	5364
Ile Lys Thr Gly Glu Trp Lys	Lys Gly Asn Cys Glu	Val Ser Ser	
1775	1780	1785	
gtg gaa gga aca cta tgc aaa	aca gct atc cca tac	aaa agg aaa	5409
Val Glu Gly Thr Leu Cys Lys	Thr Ala Ile Pro Tyr	Lys Arg Lys	
1790	1795	1800	
tat tta tca gat aac cac att	tta ata tca gca ttg	gtg att gct	5454
Tyr Leu Ser Asp Asn His Ile	Leu Ile Ser Ala Leu	Val Ile Ala	
1805	1810	1815	
agc acg gta att ttg aca gtt	ttg gga gca atc att	tgg ttc ctg	5499
Ser Thr Val Ile Leu Thr Val	Leu Gly Ala Ile Ile	Trp Phe Leu	
1820	1825	1830	
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Tyr Lys Lys His Ser Asp Ser	Arg Phe Thr Thr Val	Phe Ser Thr	
1835	1840	1845	

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 1850 1855 1860

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 35 40 45

Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
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Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
 65 70 75 80

Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
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Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
 100 105 110

His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
 115 120 125

His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
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Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg
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Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
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Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro
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Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile
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Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
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Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp
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Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser
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Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile
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Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly
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Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro
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Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met
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Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu
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Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp
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Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn
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Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys
370 375 380

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Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His
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Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp
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Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr
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Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys
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Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys
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Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys
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Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe
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Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr
 770 775 780

Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr
 785 790 795 800

Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu
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Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn
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1670						1675					1680			

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Asp Ile	Leu Leu Gly Met	Phe	Tyr Asp Thr Asp Asp	Ala Ser Phe
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Lys Trp	Phe Asp Asn Ser	Asn	Met Thr Phe Asp Lys	Trp Thr Asp
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Gln Asp	Asp Asp Glu Asp	Leu	Val Asp Thr Cys Ala	Phe Leu His
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Tyr Leu	Ser Asp Asn His	Ile	Leu Ile Ser Ala Leu	Val Ile Ala
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Ser Thr	Val Ile Leu Thr	Val	Leu Gly Ala Ile Ile	Trp Phe Leu
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Tyr Lys	Lys His Ser Asp	Ser	Arg Phe Thr Thr Val	Phe Ser Thr
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3740

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 Thr Ala Ile Val Ala Asp Cys Pro Ser Ser Thr Trp Val Gln Phe Gln
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 Gly Ser Cys Tyr Ala Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile
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 Glu Asp Val Arg Lys Gln Cys Thr Asp His Gly Ala Asp Met Val Ser
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 Arg Trp Lys Gly Pro Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr
 80 85 90 95
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 Asp Asp Ala Thr Phe Lys Trp Tyr Asp His Ser Asn Met Thr Phe Asp
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Asp Val Arg Lys Gln Cys Thr Asp His Gly Ala Asp Met Val Ser Ile
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<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> The 'Xaa' at location 5 stands for Leu.

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> The 'Xaa' at location 13 stands for Ala, or Val.

<220>
 <221> misc_feature
 <222> (142)..(142)
 <223> The 'Xaa' at location 142 stands for Thr.

<400> 11

His Glu Ala Ser Xaa Val Leu Leu Ser Leu Ala Thr Xaa Ile Phe Ala
 1 5 10 15

Asp Cys Pro Ser Ser Ile Trp Val Gln Phe Gln Gly Ser Cys Tyr Thr
 20 25 30

Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu Asp Val Arg Lys
 35 40 45

Gln Cys Thr Asp His Gly Ala Asp Leu Val Ser Ile His Asn Glu Glu
 50 55 60

Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg Trp Lys Gly Pro
 65 70 75 80

Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe
 85 90 95

Lys Trp Phe Asp Gln Ser Asn Met Thr Phe Asp Lys Trp Ala Asp Glu
 100 105 110

Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu Tyr Ala Lys Thr
 115 120 125

Gly Glu Trp Arg Lys Gly Asn Cys Glu Met Ser Ser Val Xaa Gly Thr
 130 135 140

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Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn
 145 150 155 160

His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala
 165 170 175

Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser
 180 185 190

Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly
 195 200 205

Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp
 210 215 220

<210> 12
 <211> 979
 <212> DNA
 <213> mammalian

<400> 12
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 cttttgtatc tcttacagtc tttcgtcaca tgactagtgc cccgtctgga ccattcatat 180
 gtgttacttc ttcttttgog taaatatgac ctgtgaaatg ttttcgctac ctttcggggc 240
 ctactagaag acgatccgta caaaatactg tgactactac gttcaaagtt caccaaacta 300
 gtcagtttat actgtaagct gttcaccogt ctactcctac cactcctgga tcaactgtgg 360
 acaccaaaaag acatacgggt ctgtccactt acctcttttc ctttaacact ttacagaaga 420
 cactgycctt gtgaaacggt ttgtcgtag ggtatactgt tcttcataaa tagtctattg 480
 gtgtaaaatt atagctgaga ccactagcga tcgtgtcact gagaccgtca aaaccctcgc 540
 cagtaaacca aggagatata ttcctcgcgt gcgagaccga agtggagaaa gagaggacgt 600
 ggtgttagtg gaatgtcact accgacacga gaccatcaac gccttcttct acttatgaga 660
 caagtcgacc tgactctcaa accctttag tagtctcgtg tgacttgtgg aactgttctt 720
 tattaaagga tacgttctaa cagtacattt taaacggtgc cttttgactt ggaaaatacc 780
 ataaggaata agaagattgt tataaaagta cataagttac actgttttgt atttggaaga 840
 ctaattttcc tttttttcat ccaaagtctt ttccttgatc gtgtctcgat tgaatgtcca 900

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aaagaattca tcaaaagtaa actcattttac ttctgatgtc atgttatttc gaccattttg 960
cgtttttttt tttttttttt 979

<210> 13
<211> 483
<212> DNA
<213> mammalian

<220>
<221> misc_feature
<222> (43)..(43)
<223> n is any nucleic acid

<400> 13
gagctagttg acacctgtgc ctttttgcac accaagacag gtngattgga aaaaaggaaa 60
ctgtgaagtt tcttctgtgg aaggaaccct ttgtaaagca gctatcccat atgaaaagaa 120
atatttatca gataaccgca ttttaatatc agctttgggtg attgctagca cagtaattct 180
gacagttctg ggagcagttg tttggttcct gtacaaaaga agtttggatt ctggtttcac 240
cacagttttt tcagctgcac accaatcacc ttataatgat gactgtgttt tagtagttgc 300
agaggaaaac gaatatgata ttcaatttaa ctaagatttt ggaaatatca gactaagaca 360
aatacctttc agtgattcct ctgtaagatt tcaatataaa acctgataat gaaaattagt 420
ttttatgata tattacctta ttccagtaac attcattact cttatgtaaa atcactgatc 480
atg 483

<210> 14
<211> 27
<212> DNA
<213> mammalian

<220>
<221> CDS
<222> (1)..(27)
<223>

<400> 14
aaa gtg cct ctg ggc cct gat tac aca 27
Lys Val Pro Leu Gly Pro Asp Tyr Thr
1 5

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<210> 15
 <211> 9
 <212> PRT
 <213> mammalian

<400> 15

Lys Val Pro Leu Gly Pro Asp Tyr Thr
 1 5

<210> 16
 <211> 42
 <212> DNA
 <213> mammalian

<220>
 <221> CDS
 <222> (1)..(42)
 <223>

<400> 16
 aaa gtg cct ctg gac tgt cct tca tct act tgg att cag ttc
 Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe 42
 1 5 10

<210> 17
 <211> 14
 <212> PRT
 <213> mammalian

<400> 17

Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
 1 5 10

<210> 18
 <211> 42
 <212> DNA
 <213> mammalian

<220>
 <221> CDS
 <222> (1)..(42)
 <223>

<400> 18
 gct gcc gtc gcg gac tgt cct tca tct act tgg att cag ttc
 Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe 42
 1 5 10

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<210> 19
 <211> 14
 <212> PRT
 <213> mammalian

<400> 19

Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
 1 5 10

<210> 20
 <211> 5454
 <212> DNA
 <213> mammalian
 <220>
 <221> CDS
 <222> (1)..(5451)
 <223>

<400> 20

atg agg aca ggc tgg gcg acc cct cgc cgc ccg gcg ggg ctc ctc atg	48
Met Arg Thr Gly Trp Ala Thr Pro Arg Arg Pro Ala Gly Leu Leu Met	
1 5 10 15	
ctg ctc ttc tgg ttc ttc gat ctc gcg gag ccc tct ggc cgc gca gct	96
Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala	
20 25 30	
aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag	144
Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys	
35 40 45	
cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac	192
Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp	
50 55 60	
aag tta tgg aag tgg gtg tcc cag cat cgg ctc ttt cat ttg cac tcc	240
Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser	
65 70 75 80	
caa aag tgc ctt ggc ctc gat att acc aaa tcg gta aat gag ctg aga	288
Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg	
85 90 95	
atg ttc agc tgt gac tcc agt gcc atg ctg tgg tgg aaa tgt gag cac	336
Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His	
100 105 110	
cac tct ctg tac gga gct gcc cgg tac cgg ctg gct ctg aag gat gga	384
His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly	
115 120 125	

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cat ggc aca gca atc tca aat gca tct gat gtc tgg aag aaa gga ggc His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly 130 135 140	432
tca gag gaa agc ctt tgt gac cag cct tat cat gag atc tat acc aga Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg 145 150 155 160	480
gat ggg aac tct tat ggg aga cct tgt gaa ttt cca ttc tta att gat Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp 165 170 175	528
ggg acc tgg cat cat gat tgc att ctt gat gaa gat cat agt ggg cca Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro 180 185 190	576
tgg tgt gcc acc acc tta aat tat gaa tat gac cga aag tgg ggc atc Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile 195 200 205	624
tgc tta aag cct gaa aac ggt tgt gaa gat aat tgg gaa aag aac gag Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu 210 215 220	672
cag ttt gga agt tgc tac caa ttt aat act cag acg gct ctt tct tgg Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp 225 230 235 240	720
aaa gaa gct tat gtt tca tgt cag aat caa gga gct gat tta ctg agc Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser 245 250 255	768
atc aac agt gct gct gaa tta act tac ctt aaa gaa aaa gaa ggc att Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile 260 265 270	816
gct aag att ttc tgg att ggt tta aat cag cta tac tct gct aga ggc Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly 275 280 285	864
tgg gaa tgg tca gac cac aaa cca tta aac ttt ctc aac tgg gat cca Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro 290 295 300	912
gac agg ccc agt gca cct act ata ggt ggc tcc agc tgt gca aga atg Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met 305 310 315 320	960
gat gct gag tct ggt ctg tgg cag agc ttt tcc tgt gaa gct caa ctg Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu 325 330 335	1008
ccc tat gtc tgc agg aaa cca tta aat aat aca gtg gag tta aca gat Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp 340 345 350	1056

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gtc tgg aca tac tca gat acc cgc tgt gat gca ggc tgg ctg cca aat Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn 355 360 365	1104
aat gga ttt tgc tat ctg ctg gta aat gaa agt aat tcc tgg gat aag Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys 370 375 380	1152
gca cat gcg aaa tgc aaa gcc ttc agt agt gac cta atc agc att cat Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His 385 390 395 400	1200
tct cta gca gat gtg gag gtg gtt gtc aca aaa ctc cat aat gag gat Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp 405 410 415	1248
atc aaa gaa gaa gtg tgg ata ggc ctt aag aac ata aac ata cca act Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr 420 425 430	1296
tta ttt cag tgg tca gat ggt act gaa gtt act cta aca tat tgg gat Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp 435 440 445	1344
gag aat gag cca aat gtt ccc tac aat aag acg ccc aac tgt gtt tcc Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser 450 455 460	1392
tac tta gga gag cta ggt cag tgg aaa gtc caa tca tgt gag gag aaa Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys 465 470 475 480	1440
cta aaa tat gta tgc aag aga aag gga gaa aaa ctg aat gac gca agt Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser 485 490 495	1488
tct gat aag atg tgt cct cca gat gag ggc tgg aag aga cat gga gaa Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu 500 505 510	1536
acc tgt tac aag att tat gag gat gag gtc cct ttt gga aca aac tgc Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys 515 520 525	1584
aat ctg act atc act agc aga ttt gag caa gaa tac cta aat gat ttg Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu 530 535 540	1632
atg aaa aag tat gat aaa tct cta aga aaa tac ttc tgg act ggc ctg Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu 545 550 555 560	1680
aga gat gta gat tct tgt gga gag tat aac tgg gca act gtt ggt gga Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly 565 570 575	1728

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aga agg cgg gct gta acc ttt tcc aac tgg aat ttt ctt gag cca gct	1776
Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala	
580 585 590	
tcc ccg ggc ggc tgc gtg gct atg tct act gga aag tct gtt gga aag	1824
Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys	
595 600 605	
tgg gag gtg aag gac tgc aga agc ttc aaa gca ctt tca att tgc aag	1872
Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys	
610 615 620	
aaa atg agt gga ccc ctt ggg cct gaa gaa gca tcc cct aag cct gat	1920
Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp	
625 630 635 640	
gac ccc tgt cct gaa ggc tgg cag agt ttc ccc gca agt ctt tct tgt	1968
Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys	
645 650 655	
tat aag gta ttc cat gca gaa aga att gta aga aag agg aac tgg gaa	2016
Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu	
660 665 670	
gaa gct gaa cga ttc tgc caa gcc ctt gga gca cac ctt tct agc ttc	2064
Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe	
675 680 685	
agc cat gtg gat gaa ata aag gaa ttt ctt cac ttt tta acg gac cag	2112
Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln	
690 695 700	
ttc agt ggc cag cat tgg ctg tgg att ggt ttg aat aaa agg agc cca	2160
Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro	
705 710 715 720	
gat tta caa gga tcc tgg caa tgg agt gat cgt aca cca gtg tct act	2208
Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr	
725 730 735	
att atc atg cca aat gag ttt cag cag gat tat gac atc aga gac tgt	2256
Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys	
740 745 750	
gct gct gtc aag gta ttt cat agg cca tgg cga aga ggc tgg cat ttc	2304
Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe	
755 760 765	
tat gat gat aga gaa ttt att tat ttg agg cct ttt gct tgt gat aca	2352
Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr	
770 775 780	
aaa ctt gaa tgg gtg tgc caa att cca aaa ggc cgt act cca aaa aca	2400
Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr	
785 790 795 800	

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cca gac tgg tac aat cca gac cgt gct gga att cat gga cct cca ctt Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu 805 810 815	2448
ata att gaa gga agt gaa tat tgg ttt gtt gct gat ctt cac cta aac Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn 820 825 830	2496
tat gaa gaa gcc gtc ctg tac tgt gcc agc aat cac agc ttt ctt gcg Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala 835 840 845	2544
act ata aca tct ttt gtg gga cta aaa gcc atc aaa aac aaa ata gca Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala 850 855 860	2592
aat ata tct ggt gat gga cag aag tgg tgg ata aga att agc gag tgg Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp 865 870 875 880	2640
cca ata gat gat cat ttt aca tac tca cga tat cca tgg cac cgc ttt Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe 885 890 895	2688
cct gtg aca ttt gga gag gaa tgc ttg tac atg tct gcc aag act tgg Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp 900 905 910	2736
ctt atc gac tta ggt aaa cca aca gac tgt agt acc aag ttg ccc ttc Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe 915 920 925	2784
atc tgt gaa aaa tat aat gtt tct tgc tta gag aaa tac agc cca gat Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp 930 935 940	2832
tct gca gct aaa gtg caa tgt tct gag caa tgg att cct ttt cag aat Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn 945 950 955 960	2880
aag tgt ttt cta aag atc aaa ccc gtg tct ctc aca ttt tct caa gca Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala 965 970 975	2928
agc gat acc tgt cac tcc tat ggt ggc acc ctt cct tca gtg ttg agc Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser 980 985 990	2976
cag att gaa caa gac ttt att aca tcc ttg ctt ccg gat atg gaa gct Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala 995 1000 1005	3024
act tta tgg att ggt ttg cgc tgg act gcc tat gaa aag ata aac Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn 1010 1015 1020	3069

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aaa tgg Lys Trp 1025	aca gat aac aga gag Thr Asp Asn Arg Glu 1030	ctg acg tac agt aac Leu Thr Tyr Ser Asn 1035	ttt cac cca Phe His Pro	3114
tta ttg Leu Leu 1040	ggt agt ggg agg ctg Val Ser Gly Arg Leu 1045	aga ata cca gaa aat Arg Ile Pro Glu Asn 1050	ttt ttt gag Phe Phe Glu	3159
gaa gag Glu Glu 1055	tct cgc tac cac tgt Ser Arg Tyr His Cys 1060	gcc cta ata ctc aac Ala Leu Ile Leu Asn 1065	ctc caa aaa Leu Gln Lys	3204
tca ccg Ser Pro 1070	ttt act ggg acg tgg Phe Thr Gly Thr Trp 1075	aat ttt aca tcc tgc Asn Phe Thr Ser Cys 1080	agt gaa cgc Ser Glu Arg	3249
cac ttt His Phe 1085	gtg tct ctc tgt cag Val Ser Leu Cys Gln 1090	aaa tat tca gaa gtt Lys Tyr Ser Glu Val 1095	aaa agc aga Lys Ser Arg	3294
cag acg Gln Thr 1100	ttg cag aat gct tca Leu Gln Asn Ala Ser 1105	gaa act gta aag tat Glu Thr Val Lys Tyr 1110	cta aat aat Leu Asn Asn	3339
ctg tac Leu Tyr 1115	aaa ata atc cca aag Lys Ile Ile Pro Lys 1120	act ctg act tgg cac Thr Leu Thr Trp His 1125	agt gct aaa Ser Ala Lys	3384
agg gag Arg Glu 1130	tgt ctg aaa agt aac Cys Leu Lys Ser Asn 1135	atg cag ctg gtg agc Met Gln Leu Val Ser 1140	atc acg gac Ile Thr Asp	3429
cct tac Pro Tyr 1145	cag cag gca ttc ctc Gln Gln Ala Phe Leu 1150	agt gtg cag gcg ctc Ser Val Gln Ala Leu 1155	ctt cac aac Leu His Asn	3474
tct tcc Ser Ser 1160	tta tgg atc gga ctc Leu Trp Ile Gly Leu 1165	ttc agt caa gat gat Phe Ser Gln Asp Asp 1170	gaa ctc aac Glu Leu Asn	3519
ttt ggt Phe Gly 1175	tgg tca gat ggg aaa Trp Ser Asp Gly Lys 1180	cgt ctt cat ttt agt Arg Leu His Phe Ser 1185	cgc tgg gct Arg Trp Ala	3564
gaa act Glu Thr 1190	aat ggg caa ctc gaa Asn Gly Gln Leu Glu 1195	gac tgt gta gta tta Asp Cys Val Val Leu 1200	gac act gat Asp Thr Asp	3609
gga ttc Gly Phe 1205	tgg aaa aca gtt gat Trp Lys Thr Val Asp 1210	tgc aat gac aat caa Cys Asn Asp Asn Gln 1215	cca ggt gct Pro Gly Ala	3654
att tgc Ile Cys 1220	tac tat tca gga aat Tyr Tyr Ser Gly Asn 1225	gag act gaa aaa gag Glu Thr Glu Lys Glu 1230	gtc aaa cca Val Lys Pro	3699

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gtt gac agt gtt aaa tgt cca tct cct gtt cta aat act ccg tgg Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp 1235 1240 1245	3744
ata cca ttt cag aac tgt tgc tac aat ttc ata ata aca aag aat Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Ile Thr Lys Asn 1250 1255 1260	3789
agg cat atg gca aca aca cag gat gaa gtt cat act aaa tgc cag Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln 1265 1270 1275	3834
aaa ctg aat cca aaa tca cat att ctg agt att cga gat gaa aag Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys 1280 1285 1290	3879
gag aat aac ttt gtt ctt gag caa ctg ctg tac ttc aat tat atg Glu Asn Asn Phe Val Leu Glu Gln Leu Leu Tyr Phe Asn Tyr Met 1295 1300 1305	3924
gct tca tgg gtc atg tta gga ata act tat aga aat aat tct ctt Ala Ser Trp Val Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu 1310 1315 1320	3969
atg tgg ttt gat aag acc cca ctg tca tat aca cat tgg aga gca Met Trp Phe Asp Lys Thr Pro Leu Ser Tyr Thr His Trp Arg Ala 1325 1330 1335	4014
gga aga cca act ata aaa aat gag aag ttt ttg gct ggt tta agt Gly Arg Pro Thr Ile Lys Asn Glu Lys Phe Leu Ala Gly Leu Ser 1340 1345 1350	4059
act gac ggc ttc tgg gat att caa acc ttt aaa gtt att gaa gaa Thr Asp Gly Phe Trp Asp Ile Gln Thr Phe Lys Val Ile Glu Glu 1355 1360 1365	4104
gca gtt tat ttt cac cag cac agc att ctt gct tgt aaa att gaa Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys Lys Ile Glu 1370 1375 1380	4149
atg gtt gac tac aaa gaa gaa cat aat act aca ctg cca cag ttt Met Val Asp Tyr Lys Glu Glu His Asn Thr Thr Leu Pro Gln Phe 1385 1390 1395	4194
atg cca tat gaa gat ggt att tac agt gtt att caa aaa aag gta Met Pro Tyr Glu Asp Gly Ile Tyr Ser Val Ile Gln Lys Lys Val 1400 1405 1410	4239
aca tgg tat gaa gca tta aac atg tgt tct caa agt gga ggt cac Thr Trp Tyr Glu Ala Leu Asn Met Cys Ser Gln Ser Gly Gly His 1415 1420 1425	4284
ttg gca agc gtt cac aac caa aat ggc cag ctc ttt ctg gaa gat Leu Ala Ser Val His Asn Gln Asn Gly Gln Leu Phe Leu Glu Asp 1430 1435 1440	4329

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att gta Ile Val 1445	aaa cgt Lys Arg	gat gga Asp Gly	ttt phe Phe 1450	cca cta Pro Leu	tgg gtt Trp Val	ggg gtc Gly Leu	ctc tca Ser Ser	agt Ser	4374
cat gat His Asp 1460	gga agt Gly Ser	gaa tca Glu Ser	agt ser Ser 1465	ttt gaa Phe Glu	tgg tct Trp Ser	gat asp Asp 1470	ggg agt Gly Ser	aca thr Thr	4419
ttt gac Phe Asp 1475	tat atc Tyr Ile	cca tgg Pro Trp	aaa lys Lys 1480	ggc caa Gly Gln	aca tct Thr Ser	cct pro Pro 1485	gga aat Gly Asn	tgt cys Cys	4464
gtt ctc Val Leu 1490	ttg gat Leu Asp	cca aaa Pro Lys	gga gly Gly 1495	act tgg Thr Trp	aaa cat Lys His	gaa glu Glu 1500	aaa tgc Lys Cys	aac asn Asn	4509
tct gtt Ser Val 1505	aag gat Lys Asp	ggt gct Gly Ala	att ile Ile 1510	tgt tat Cys Tyr	aaa cct Lys Pro	aca thr Thr 1515	aaa tct Lys Ser	aaa lys Lys	4554
aag ctg Lys Leu 1520	tcc cgt Ser Arg	ctt aca Leu Thr	tat tyr Tyr 1525	tca tca Ser Ser	aga tgt Arg Cys	cca pro Pro 1530	gca gca Ala Ala	aaa lys Lys	4599
gag aat Glu Asn 1535	ggg tca Gly Ser	cgg tgg Arg Trp	atc ile Ile 1540	cag tac Gln Tyr	aag ggt Lys Gly	cac his His 1545	tgt tac Cys Tyr	aag lys Lys	4644
tct gat Ser Asp 1550	cag gca Gln Ala	ttg cac Leu His	agt ser Ser 1555	ttt tca Phe Ser	gag gcc Glu Ala	aaa lys Lys 1560	aaa ttg Lys Leu	tgt cys Cys	4689
tca aaa Ser Lys 1565	cat gat His Asp	cac tct His Ser	gca ala Ala 1570	act atc Thr Ile	gtt tcc Val Ser	ata ile Ile 1575	aaa gat Lys Asp	gaa glu Glu	4734
gat gag Asp Glu 1580	aat aaa Asn Lys	ttt gtg Phe Val	agc ser Ser 1585	aga ctg Arg Leu	atg agg Met Arg	gaa glu Glu 1590	aat aat Asn Asn	aac asn Asn	4779
att acc Ile Thr 1595	atg aga Met Arg	gtt tgg Val Trp	ctt leu Leu 1600	gga tta Gly Leu	tct caa Ser Gln	cat his His 1605	tct gtt Ser Val	gac asp Asp	4824
tgt cct Cys Pro 1610	tca tct Ser Ser	act tgg Thr Trp	att ile Ile 1615	cag ttc Gln Phe	caa gac Gln Asp	agt ser Ser 1620	tgt tac Cys Tyr	att ile Ile	4869
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aat cag Asn Gln 1640	tgt act Cys Thr	gac cat Asp His	gga gly Gly 1645	gcg gac Ala Asp	atg ata Met Ile	agc ser Ser 1650	ata cat Ile His	aat asn Asn	4959

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gaa gaa gaa aat gct ttt ata ctg gat act ttg aaa aag caa tgg	5004
Glu Glu Glu Asn Ala Phe Ile Leu Asp Thr Leu Lys Lys Gln Trp	
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aaa ggc cca gat gat atc cta cta ggc atg ttt tat gac aca gat	5049
Lys Gly Pro Asp Asp Ile Leu Leu Gly Met Phe Tyr Asp Thr Asp	
1670 1675 1680	
gat gcg agt ttc aag tgg ttt gat aat tca aat atg aca ttt gat	5094
Asp Ala Ser Phe Lys Trp Phe Asp Asn Ser Asn Met Thr Phe Asp	
1685 1690 1695	
aag tgg aca gac caa gat gat gat gag gat tta gtt gac acc tgt	5139
Lys Trp Thr Asp Gln Asp Asp Asp Glu Asp Leu Val Asp Thr Cys	
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gct ttt ctg cac atc aag aca ggt gaa tgg aaa aaa gga aat tgt	5184
Ala Phe Leu His Ile Lys Thr Gly Glu Trp Lys Lys Gly Asn Cys	
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gaa gtt tct tct gtg gaa gga aca cta tgc aaa aca gct atc cca	5229
Glu Val Ser Ser Val Glu Gly Thr Leu Cys Lys Thr Ala Ile Pro	
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tac aaa agg aaa tat tta tca gat aac cac att tta ata tca gca	5274
Tyr Lys Arg Lys Tyr Leu Ser Asp Asn His Ile Leu Ile Ser Ala	
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Leu Val Ile Ala Ser Thr Val Ile Leu Thr Val Leu Gly Ala Ile	
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att tgg ttc ctg tac aaa aaa cat tct gat tct cgt ttc acc aca	5364
Ile Trp Phe Leu Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr	
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gtt ttt tca acc gca ccc caa tca cct tat aat gaa gac tgt gtt	5409
Val Phe Ser Thr Ala Pro Gln Ser Pro Tyr Asn Glu Asp Cys Val	
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ttg gta gtt gga gaa gaa aat gaa tat cct gtt caa ttt gac taa	5454
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 <213> mammalian

<400> 21

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Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys
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Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
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Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
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Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
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Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
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His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
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His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
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Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg
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Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
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Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro
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Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile
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Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
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Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp
 225 230 235 240

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Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser
245 250 255

Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile
260 265 270

Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly
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Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro
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Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met
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Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu
325 330 335

Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp
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Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn
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Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys
370 375 380

Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His
385 390 395 400

Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp
405 410 415

Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr
420 425 430

Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp
435 440 445

Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser
450 455 460

- 49 -

Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys
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Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser
 485 490 495

Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu
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Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys
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Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu
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Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu
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Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly
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Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala
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Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys
 595 600 605

Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys
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Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp
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Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys
 645 650 655

Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu
 660 665 670

Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe
 675 680 685

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Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln
 690 695 700

Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro
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Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr
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Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys
 740 745 750

Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe
 755 760 765

Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr
 770 775 780

Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr
 785 790 795 800

Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu
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Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn
 820 825 830

Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala
 835 840 845

Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala
 850 855 860

Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp
 865 870 875 880

Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe
 885 890 895

Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp
 900 905 910

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Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe
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Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp
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Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn
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Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala
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Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser
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Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala
 995 1000 1005

Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn
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Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu
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Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys
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Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg
 1070 1075 1080

His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg
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Gln Thr Leu Gln Asn Ala Ser Glu Thr Val Lys Tyr Leu Asn Asn
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Leu Tyr Lys Ile Ile Pro Lys Thr Leu Thr Trp His Ser Ala Lys
 1115 1120 1125

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Arg Glu Cys Leu Lys Ser Asn Met Gln Leu Val Ser Ile Thr Asp
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Pro Tyr Gln Gln Ala Phe Leu Ser Val Gln Ala Leu Leu His Asn
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Ser Ser Leu Trp Ile Gly Leu Phe Ser Gln Asp Asp Glu Leu Asn
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Phe Gly Trp Ser Asp Gly Lys Arg Leu His Phe Ser Arg Trp Ala
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Glu Thr Asn Gly Gln Leu Glu Asp Cys Val Val Leu Asp Thr Asp
 1190 1195 1200

Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro Gly Ala
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Ile Cys Tyr Tyr Ser Gly Asn Glu Thr Glu Lys Glu Val Lys Pro
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Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp
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Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Ile Thr Lys Asn
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Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln
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Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys
 1280 1285 1290

Glu Asn Asn Phe Val Leu Glu Gln Leu Leu Tyr Phe Asn Tyr Met
 1295 1300 1305

Ala Ser Trp Val Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu
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Met Trp Phe Asp Lys Thr Pro Leu Ser Tyr Thr His Trp Arg Ala
 1325 1330 1335

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Gly Arg Pro Thr Ile Lys Asn Glu Lys Phe Leu Ala Gly Leu Ser
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Thr Asp Gly Phe Trp Asp Ile Gln Thr Phe Lys Val Ile Glu Glu
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Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys Lys Ile Glu
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Met Val Asp Tyr Lys Glu Glu His Asn Thr Thr Leu Pro Gln Phe
 1385 1390 1395

Met Pro Tyr Glu Asp Gly Ile Tyr Ser Val Ile Gln Lys Lys Val
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Thr Trp Tyr Glu Ala Leu Asn Met Cys Ser Gln Ser Gly Gly His
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Leu Ala Ser Val His Asn Gln Asn Gly Gln Leu Phe Leu Glu Asp
 1430 1435 1440

Ile Val Lys Arg Asp Gly Phe Pro Leu Trp Val Gly Leu Ser Ser
 1445 1450 1455

His Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser Asp Gly Ser Thr
 1460 1465 1470

Phe Asp Tyr Ile Pro Trp Lys Gly Gln Thr Ser Pro Gly Asn Cys
 1475 1480 1485

Val Leu Leu Asp Pro Lys Gly Thr Trp Lys His Glu Lys Cys Asn
 1490 1495 1500

Ser Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro Thr Lys Ser Lys
 1505 1510 1515

Lys Leu Ser Arg Leu Thr Tyr Ser Ser Arg Cys Pro Ala Ala Lys
 1520 1525 1530

Glu Asn Gly Ser Arg Trp Ile Gln Tyr Lys Gly His Cys Tyr Lys
 1535 1540 1545

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1565						1570					1575			
Asp	Glu	Asn	Lys	Phe	Val	Ser	Arg	Leu	Met	Arg	Glu	Asn	Asn	Asn
1580						1585					1590			
Ile	Thr	Met	Arg	Val	Trp	Leu	Gly	Leu	Ser	Gln	His	Ser	Val	Asp
1595						1600					1605			
Cys	Pro	Ser	Ser	Thr	Trp	Ile	Gln	Phe	Gln	Asp	Ser	Cys	Tyr	Ile
1610						1615					1620			
Phe	Leu	Gln	Glu	Ala	Ile	Lys	Val	Glu	Ser	Ile	Glu	Asp	Val	Arg
1625						1630					1635			
Asn	Gln	Cys	Thr	Asp	His	Gly	Ala	Asp	Met	Ile	Ser	Ile	His	Asn
1640						1645					1650			
Glu	Glu	Glu	Asn	Ala	Phe	Ile	Leu	Asp	Thr	Leu	Lys	Lys	Gln	Trp
1655						1660					1665			
Lys	Gly	Pro	Asp	Asp	Ile	Leu	Leu	Gly	Met	Phe	Tyr	Asp	Thr	Asp
1670						1675					1680			
Asp	Ala	Ser	Phe	Lys	Trp	Phe	Asp	Asn	Ser	Asn	Met	Thr	Phe	Asp
1685						1690					1695			
Lys	Trp	Thr	Asp	Gln	Asp	Asp	Asp	Glu	Asp	Leu	Val	Asp	Thr	Cys
1700						1705					1710			
Ala	Phe	Leu	His	Ile	Lys	Thr	Gly	Glu	Trp	Lys	Lys	Gly	Asn	Cys
1715						1720					1725			
Glu	Val	Ser	Ser	Val	Glu	Gly	Thr	Leu	Cys	Lys	Thr	Ala	Ile	Pro
1730						1735					1740			
Tyr	Lys	Arg	Lys	Tyr	Leu	Ser	Asp	Asn	His	Ile	Leu	Ile	Ser	Ala
1745						1750					1755			

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Leu Val Ile Ala Ser Thr Val Ile Leu Thr Val Leu Gly Ala Ile
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Ile Trp Phe Leu Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr
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Val Phe Ser Thr Ala Pro Gln Ser Pro Tyr Asn Glu Asp Cys Val
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